

In the Specification:

Please replace the paragraph beginning at page 6, line 31, with the following:

--Figure 1: Figure 1 provides an amino acid alignment of Kv10.1 (SEQ ID NO:3) with Kv2.1 (SEQ ID NO:12) and Kv2.2 (SEQ ID NO:13). Identical amino acids are shaded, and amino acid position is given at the left margin. Gaps in the alignment are indicated by dashes.--

Please replace the paragraph beginning at page 7, line 1, with the following:

--Figure 2: Figure 2 provides an amino acid alignment of the S6 domains of Kv10.1 (SEQ ID NO:14), Kv6.1 (SEQ ID NO:15) and Kv2.1 (SEQ ID NO:16). Arrows mark two residues that typically differ between normal Kv family polypeptides that form functional channels as homomultimers and electrically silent Kv channel polypeptides that form functional channels as heteromultimers. These residues are always glycine (G) and proline (P), respectively, in Kv subunits that express as homotetramers. Kv10.1 differs at these residues, much like the electrically silent subunit Kv6.1.--

Please replace the paragraph beginning at page 27, line 23, with the following:

--In general, the nucleic acid sequences encoding Kv10.1 and related nucleic acid sequence homologs such as other Kv10 subfamily members are cloned from cDNA and genomic DNA libraries or isolated using amplification techniques with oligonucleotide primers. For example, Kv10.1 sequences are typically isolated from human nucleic acid (genomic or cDNA) libraries by hybridizing with a nucleic acid probe or polynucleotide, the sequence of which can be derived from SEQ ID NOS:1-2, preferably from the region encoding the conserved region (*see, e.g.*, amino acids 102 to